

# SEQUENCE LISTING

<110> Shi, Jinrui  
Beach, Larry  
Wang, Hongyu  
Rafalski, Antoni J.  
Rebecca E. Cahoon

<120> Novel Inositol Polyphosphate Kinase  
Genes and Uses Thereof

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<151> 2001-01-12

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Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu	
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His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro	
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 Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro  
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 Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe  
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ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298  
 Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly  
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Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro	
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Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly	
115 120 125 130	
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Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp				
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Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser	
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Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val Tyr Gly	
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Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly	
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Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Gly Val Thr	
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Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile	
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Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser	
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Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe  
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Leu	Gln	Ala	Gly	Asp	Arg	Gly	Glu	His	Glu	Val	Ala	Phe	Tyr	Glu	Ala		
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Met	Asp	Thr	Ala	Gly	Val	Arg	Arg	Val	Leu	Arg	Arg	Tyr	Val	Ser	Ser		
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Gly	Lys	Gly	Gly	Val	Leu	Ser	Gln	Leu	Arg	Glu	Leu	Lys	Ala	Trp	Phe		
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Glu	Glu	Gln	Thr	Leu	Phe	His	Phe	Tyr	Ser	Ala	Ser	Ile	Leu	Leu	Gly		
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Tyr	Asp	Ala	Ala	Ala	Val	Ala	Ala	Gly	Gly	Asp	Gly	Gly	Gly	Val	Thr		
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Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser  
260 265 270

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275 280 285

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Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
50 55 60  
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
65 70 75 80  
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
85 90 95  
Phe Gln Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
100 105 110  
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp  
115 120 125  
Arg Gly Thr Thr Ser Val Leu Gly Phe Arg Val Ser Gly Val Arg  
130 135 140  
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
145 150 155 160  
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
165 170 175  
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val  
180 185 190  
Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala  
195 200 205  
Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu  
210 215 220  
Leu Gly Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Gly  
225 230 235 240

Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly  
 245 250 255  
 Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe  
 260 265 270  
 Val Ser Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro  
 275 280 285  
 Ser

<210> 9  
 <211> 1105  
 <212> DNA  
 <213> Glycine max

<220>  
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 <222> (12)...(851)

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 Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys  
 1 5 10  
 gcc aag gac gga atc ctg ggc cca ctc gtc gac gat ttt gga aaa ttc 98  
 Ala Lys Asp Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe  
 15 20 25  
 tac aag ccc ctc cag acc aac aaa gac gac gac acc cgc ggc tcc acc 146  
 Tyr Lys Pro Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr  
 30 35 40 45  
 gaa ctc tcc ttt tac acc tct ctc gcc gcc gcc gcc cac gac tac tcc 194  
 Glu Leu Ser Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser  
 50 55 60  
 atc cgc tcc ttc ttc ccc gcc ttt cac ggc acc cgc ctc ctg gac gcc 242  
 Ile Arg Ser Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala  
 65 70 75  
 tcc gac ggc tcc ggt ccc cac cct cac ctg gtc ctg gag gac ctc ctc 290  
 Ser Asp Gly Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu  
 80 85 90  
 tgc ggc tac tcc aaa ccc tcc gtc atg gac gta aag atc ggc tcc aga 338  
 Cys Gly Tyr Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg  
 95 100 105  
 acc tgg cac ctg gga gac tcc gag gac tac atc tgc aag tgc ctg aag 386  
 Thr Trp His Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys  
 110 115 120 125  
 aag gac aga gag tcc tct agc ttg ccc ttg ggt ttc aga atc tcg gga 434  
 Lys Asp Arg Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly  
 130 135 140  
 gtc aag gac tct atc tcc tcc tgg gaa cct acc agg aaa tct ctc cag 482  
 Val Lys Asp Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln

10042894 010902

145	150	155	
tgt cta tcc gcc cat ggt gtt gca ctt gtt ctc aac aag ttc gtt tcc			530
Cys Leu Ser Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser			
160	165	170	
tct aat aat atc aac cat gat gat cat cat ccc gat tgc gct ttc gca			578
Ser Asn Asn Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala			
175	180	185	
acg gag gtc tac ggc gcc gtt ttg gag cgc ttg cag aag ctc aag gac			626
Thr Glu Val Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp			
190	195	200	205
tgg ttc gag gtt cag acg gtg tat cac ttc tat tct tgt tct gtt ctt			674
Trp Phe Glu Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu			
210	215	220	
gtg gtg tac gag aag gat cta ggg aaa ggg aaa gct acc aac cct ctg			722
Val Val Tyr Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu			
225	230	235	
gtc aaa ctc gtt gac ttt gca cac gtg gtg gac gga aac ggt gtc att			770
Val Lys Leu Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile			
240	245	250	
gat cac aac ttc ttg ggt ggc ctt tgt tcc ttc atc aag ttc ctc aag			818
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys			
255	260	265	
gat atc cta gca gta gca tgt ctt cac aag tga ctgattttca tcgagttaat			871
Asp Ile Leu Ala Val Ala Cys Leu His Lys *			
270	275		
cttattccta tcagaaaata attatgcttg aattagtgtc gcagactaac tgtttgaagt			931
actgtcagaa acaaaaataat aatatggact gagaggcaat cttgttctgc taaactccct			991
ttcaagttgc tgtcagatac tagccgtccc ttttcctttt tcatattctg tcaaagtgag			1051
tcattttaata ataataacaa tgtccttcaa ctccaaaaaa aaaaaaaaaa aaaa			1105
<210> 10			
<211> 279			
<212> PRT			
<213> Glycine max			
<400> 10			
Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys Ala Lys Asp			
1	5	10	15
Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro			
20	25	30	
Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser			
35	40	45	
Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser Ile Arg Ser			
50	55	60	
Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly			
65	70	75	80
Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr			
85	90	95	
Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His			

	100		105		110
Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys Lys Asp Arg					
115			120		125
Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly Val Lys Asp					
130			135		140
Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln Cys Leu Ser					
145			150		155
Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser Ser Asn Asn					
165			170		175
Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala Thr Glu Val					
180			185		190
Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp Trp Phe Glu					
195			200		205
Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu Val Val Tyr					
210			215		220
Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu Val Lys Leu					
225			230		235
Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile Asp His Asn					
245			250		255
Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys Asp Ile Leu					
260			265		270
Ala Val Ala Cys Leu His Lys					
275					

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 <211> 1195  
 <212> DNA  
 <213> Eucalyptus grandis

<220>  
 <221> CDS  
 <222> (116)...(1048)

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	Met
	1
ctc aag gtc ccg gat cat caa gtc gcc ggt cac cgg gga gac ggg gga	166
Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly Gly	
5 10 15	
aag ctg ggg cca ctg gtg gat gat tcg ggc cgc ttc tat aag cct ctc	214
Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro Leu	
20 25 30	
cag agc gat cat cgc gga gac acg gaa gtg gcc ttt tac gag tca ttc	262
Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser Phe	
35 40 45	
tat tcc aat acc gag atc cca ggt cac att cgc aaa ttc ttt cct gcg	310
Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro Ala	
50 55 60 65	
ttt cac gga act aag act att gag gcg tct gat gga tcg ggt cct caa	358
Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro Gln	

					70					75					80					
cct	cac	ctg	gtt	ctg	gag	gat	ctc	gtc	tcg	ggc	cgc	acg	aac	cca	tct		406			
Pro	His	Leu	Val	Leu	Glu	Asp	Leu	Val	Ser	Gly	Arg	Thr	Asn	Pro	Ser					
					85					90					95					
ctc	atg	gac	atc	aag	act	gga	tcc	aga	aca	tgg	tat	ccg	gag	gcc	tct		454			
Leu	Met	Asp	Ile	Lys	Thr	Gly	Ser	Arg	Thr	Trp	Tyr	Pro	Glu	Ala	Ser					
					100					105					110					
gag	gag	tac	atc	caa	aag	tgc	tta	gag	aaa	gat	cga	aat	agc	aca	agc		502			
Glu	Glu	Tyr	Ile	Gln	Lys	Cys	Leu	Glu	Lys	Asp	Arg	Asn	Ser	Thr	Ser					
					115					120					125					
gtt	tca	ttg	ggc	ttt	agg	att	tct	ggg	cta	agg	gta	tat	caa	aat	agc		550			
Val	Ser	Leu	Gly	Phe	Arg	Ile	Ser	Gly	Leu	Arg	Val	Tyr	Gln	Asn	Ser					
					130					135					140					145
gaa	gct	gga	ttt	tgg	caa	cct	gag	aag	aag	gtt	gtt	tat	agc	ttt	aat		598			
Glu	Ala	Gly	Phe	Trp	Gln	Pro	Glu	Lys	Lys	Val	Val	Tyr	Ser	Phe	Asn					
					150					155					160					
gcg	gac	ggc	gtc	agg	tcg	gct	ctg	agg	aag	ttt	gtt	tct	tcc	aac	ttg		646			
Ala	Asp	Gly	Val	Arg	Ser	Ala	Leu	Arg	Lys	Phe	Val	Ser	Ser	Asn	Leu					
					165					170					175					
tct	ctg	ggc	cca	aat	gtg	gat	ccg	gat	tgt	ttg	tat	gca	tca	aaa	gtt		694			
Ser	Leu	Gly	Pro	Asn	Val	Asp	Pro	Asp	Cys	Leu	Tyr	Ala	Ser	Lys	Val					
					180					185					190					
tac	tgt	cac	cgg	ggc	gga	att	ttg	gca	caa	ttg	ctt	cag	ctg	aag	gaa		742			
Tyr	Cys	His	Arg	Gly	Gly	Ile	Leu	Ala	Gln	Leu	Leu	Gln	Leu	Lys	Glu					
					195					200					205					
tgg	ttt	gag	gtt	cag	acg	aat	tat	cac	ttc	tat	tct	tgt	tca	ctc	att		790			
Trp	Phe	Glu	Val	Gln	Thr	Asn	Tyr	His	Phe	Tyr	Ser	Cys	Ser	Leu	Ile					
					210					215					220					225
atc	tta	tat	gac	agg	gag	tct	gct	ttg	gac	ggc	tgt	gca	cac	ccg	aaa		838			
Ile	Leu	Tyr	Asp	Arg	Glu	Ser	Ala	Leu	Asp	Gly	Cys	Ala	His	Pro	Lys					
					230					235					240					
gtt	aaa	ctg	gtg	gac	ttt	gca	cat	gtg	atg	gat	ggc	cac	ggc	gtg	atc		886			
Val	Lys	Leu	Val	Asp	Phe	Ala	His	Val	Met	Asp	Gly	His	Gly	Val	Ile					
					245					250					255					
gat	cac	aac	ttc	ttg	ggc	ggc	ctc	tgt	tct	gta	atc	aag	ttt	ata	cgt		934			
Asp	His	Asn	Phe	Leu	Gly	Gly	Leu	Cys	Ser	Val	Ile	Lys	Phe	Ile	Arg					
					260					265					270					
gac	att	gct	gat	gaa	gat	aac	aag	tgt	gca	aag	tgc	gaa	gtc	aat	ctt		982			
Asp	Ile	Ala	Asp	Glu	Asp	Asn	Lys	Cys	Ala	Lys	Cys	Glu	Val	Asn	Leu					
					275					280					285					
gga	ttg	aaa	gaa	aat	ggc	ttc	tat	aag	agc	agc	acg	gaa	cca	gag	ctt		1030			
Gly	Leu	Lys																		

gat cac gag gcc tgc tag tggaaactgg agaataactg cattcatgca 1078  
 Asp His Glu Ala Cys \*  
 310

ttcctgcatt cctgctctga caagtgggtc agaatgggta taataacagt ctattttagt 1138  
 caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1195

<210> 12  
 <211> 310  
 <212> PRT  
 <213> Eucalyptus grandis

<400> 12  
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 1 5 10 15  
 Gly Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 20 25 30  
 Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser  
 35 40 45  
 Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro  
 50 55 60  
 Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro  
 65 70 75 80  
 Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro  
 85 90 95  
 Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala  
 100 105 110  
 Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr  
 115 120 125  
 Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn  
 130 135 140  
 Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe  
 145 150 155 160  
 Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn  
 165 170 175  
 Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys  
 180 185 190  
 Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys  
 195 200 205  
 Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu  
 210 215 220  
 Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro  
 225 230 235 240  
 Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val  
 245 250 255  
 Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile  
 260 265 270  
 Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn  
 275 280 285  
 Leu Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu  
 290 295 300  
 Leu Asp His Glu Ala Cys  
 305 310

<210> 13  
 <211> 1020  
 <212> DNA

10042894.010902

<213> Parthenium argentatum

<220>

<221> CDS

<222> (21)...(908)

<400> 13

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Met Leu Lys Ala Pro Asp His Gln Val Ala Gly  
1 5 10

cat gaa gct ggg ctc ggg aag ctt ggc cca ctc att gat gat tca ggc 101  
His Glu Ala Gly Leu Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly  
15 20 25

cgg ttt tac aaa cca ctg cag ggt gat aac cgt ggg tca gaa gaa gta 149  
Arg Phe Tyr Lys Pro Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val  
30 35 40

gcc ttt tat gaa tca ttt tct tct aac aat aat att cca gaa cac ata 197  
Ala Phe Tyr Glu Ser Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile  
45 50 55

cgc aaa ttc ttt cct ata tat tat ggc acc aaa atc atg aag gca tcc 245  
Arg Lys Phe Phe Pro Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser  
60 65 70 75

act ggc tct gac cat cct cac atg gtg ttg caa gat ctt aca tca gct 293  
Thr Gly Ser Asp His Pro His Met Val Leu Gln Asp Leu Thr Ser Ala  
80 85 90

cat gtc aac cca tct gta atg gac atc aaa atc ggg tcc aga aca tgg 341  
His Val Asn Pro Ser Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp  
95 100 105

gcg cca gaa gct tcc gag gcg tac att gca aaa tgc tta aaa aag gat 389  
Ala Pro Glu Ala Ser Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp  
110 115 120

agg gaa agc aca agt att cca ttg gga ttc agg atc tcc ggg ctg caa 437  
Arg Glu Ser Thr Ser Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln  
125 130 135

gtc tat atc gat gat ggg tca ggg ttt tat aag cct cat aga aat tac 485  
Val Tyr Ile Asp Asp Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr  
140 145 150 155

atg cgt aaa acc ggc cca gct gat gtt aga cta ctt ctt agg aaa ttt 533  
Met Arg Lys Thr Gly Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe  
160 165 170

gtt tct tct aac ccg tct gca gag atg gaa atg cgc aca ggc cta ggc 581  
Val Ser Ser Asn Pro Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly  
175 180 185

ccg gat tgt tct tta gca tct ttt gtt tat ggt ggg cct aat ggg ata 629  
Pro Asp Cys Ser Leu Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile  
190 195 200

tta gct caa ctg atg gaa ttg aag aca tgg ttt gaa gat caa aca att 677  
 Leu Ala Gln Leu Met Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile  
 205 210 215

tac cac ttc tat gct tgt tct ttt ttg ttc atc ttt gaa aag agg ttg 725  
 Tyr His Phe Tyr Ala Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu  
 220 225 230 235

gtg tta aaa ggt gct cgg tca aac gca gaa gtc aaa ctt att gat ttt 773  
 Val Leu Lys Gly Ala Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe  
 240 245 250

gct cat gtt aca gat ggt aat ggt gtt att gat cac aat ttc ttg ggt 821  
 Ala His Val Thr Asp Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly  
 255 260 265

ggg ctc tgt tct ttg ata aag ttc att tct gac ata ctt tcg gag aca 869  
 Gly Leu Cys Ser Leu Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr  
 270 275 280

aaa gat tgt aat ggt aca aac ggt cag gtt gaa ctt tga aactctcttc 918  
 Lys Asp Cys Asn Gly Thr Asn Gly Gln Val Glu Leu \*  
 285 290 295

ttgttgcttt tcttcaataa tttatcatga cagtgttttaa ttgtaaagat attcgcttac 978  
 cggaatatat cttgggtatg agtgaaaaaa aaaaaaaaaa aa 1020

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 <211> 295  
 <212> PRT  
 <213> Parthenium argentatum

<400> 14  
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 Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 20 25 30  
 Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val Ala Phe Tyr Glu Ser  
 35 40 45  
 Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile Arg Lys Phe Phe Pro  
 50 55 60  
 Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser Thr Gly Ser Asp His  
 65 70 75 80  
 Pro His Met Val Leu Gln Asp Leu Thr Ser Ala His Val Asn Pro Ser  
 85 90 95  
 Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp Ala Pro Glu Ala Ser  
 100 105 110  
 Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp Arg Glu Ser Thr Ser  
 115 120 125  
 Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln Val Tyr Ile Asp Asp  
 130 135 140  
 Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr Met Arg Lys Thr Gly  
 145 150 155 160  
 Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe Val Ser Ser Asn Pro  
 165 170 175  
 Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly Pro Asp Cys Ser Leu  
 180 185 190



Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met  
 195 200 205  
 Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala  
 210 215 220  
 Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala  
 225 230 235 240  
 Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp  
 245 250 255  
 Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu  
 260 265 270  
 Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr Lys Asp Cys Asn Gly  
 275 280 285  
 Thr Asn Gly Gln Val Glu Leu  
 290 295

<210> 15  
 <211> 899  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (89)...(424)

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 Met Pro Asp Leu His Pro Pro Glu  
 1 5  
 cac caa gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc cca ctc 160  
 His Gln Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu  
 10 15 20  
 atc gac ggc tct ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt 208  
 Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg  
 25 30 35 40  
 ggg gag cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc 256  
 Gly Glu His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala  
 45 50 55  
 gtc ccg gcc cgc atc cga gac acc ttc ttc ccc ccg ttc cac ggc acg 304  
 Val Pro Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr  
 60 65 70  
 cga ctc ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg tac ctc 352  
 Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro Tyr Leu  
 75 80 85  
 gtc ctc gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac 400  
 Val Leu Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp  
 90 95 100  
 atc aag atc ggt gcc atc acg tga ccatgagcga tctgctcgga ttccacgtct 454  
 Ile Lys Ile Gly Ala Ile Thr \*  
 105 110

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ccggcgctccg agtcgtcggc cccgagggcg ccgtgtggcg gacggagcgc cctgaggtga 514
aggctatgga cattgtcggc gtccgccggc tgctccggcg ctgcatgtca tccgcttgcc 574
ggcgagggga tggactgcgc gctcgcggcg gcggtgtacg gaggaagagg tggagtcttg 634
tcacagctgc gcgagctcaa ggcgtggttc gaggggcaga ctctgttcca cttctactcg 694
gcgtcgattc ttctgggcta tgatgctgct gcagtcgcag caggcggagg tgggggtggg 754
gtaacagtga agctgggtga ccttgcccat gtggccgagg gtgatgggt gattgaccac 814
aacttcctgg gcgggctctg ctagctgac aagtttgtt ctgacattgt tccagagact 874
ccttagacgc agcaagggcg aattc 899

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<210> 16  
 <211> 111  
 <212> PRT  
 <213> Zea mays

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<400> 16
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Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
 20          25          30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
 35          40          45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
 50          55          60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
 65          70          75          80
Pro Gly Glu Pro His Pro Tyr Leu Val Leu Asp Asp Leu Leu Ala Gly
 85          90          95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr
100          105          110

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<210> 17  
 <211> 643  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> misc\_feature  
 <222> (1)...(643)  
 <223> n = A,T,C or G

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ccgacctcca cccgcccggg caccaagtcg ccggtcaccg cgcctccgcc agcaagctgg 180
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agatcctggc	attttcgatt	tgataacaaa	ggaancactt	tcagctgcc	aaaaaaaaanc		360
accagtgag	atgaaaaata	cattatttag	gaaagttccg	atnataaccc	accanattna		420
aaaaaaaaaag	gtcccaaat	tccgaaaatn	tggactctaa	gaataatctc	ctgaaaacan		480
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<213> Zea mays
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      Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly
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 His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly  
 15 20 25

ctc ttc tac aag cgg ctc cag gcc ggc gac cgt ggg gag cac gag gtc 206  
Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val  
30 35 40 45

gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc	254
Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile	
50 55 60	
cga gac acc ttc ttc ccc cgg ttc cac ggc acg cga ctc ctc ccc acc	302
Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr	
65 70 75	
gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc gac gac ctc	350
Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu	
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ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag atc ggt gcc	398
Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala	
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Ile Thr *	
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 <212> PRT  
 <213> Zea mays

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 Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
 35 40 45  
 Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
 50 55 60  
 Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
 65 70 75 80  
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 100 105 110

<210> 22  
 <211> 1448  
 <212> DNA  
 <213> Parthenium argentatum

<220>  
 <221> CDS  
 <222> (52)...(1020)

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 Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys Asp Glu  
 5 10 15  
 cct tcc aac ccc gat cag gcg cag cac cag cct gac gag cgc gtt caa 153  
 Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg Val Gln  
 20 25 30

cac ttc atc ctt ctt gaa gac ctt act gct ggc atg aca agg cct tgt	201
His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg Pro Cys	
35 40 45 50	
gtc tta gac ttg aag atg ggt acg cgc cag tat ggt gtg gaa gcc gat	249
Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu Ala Asp	
55 60 65	
gag aag aaa cag cgg tct caa cgg cgc aag tgt cag atg acc acc agt	297
Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr Thr Ser	
70 75 80	
gct caa ctc ggc gtg cga gtc tgc ggt atg caa att tgg aac gcc aag	345
Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn Ala Lys	
85 90 95	
acc cag agc tac atc ttc gag gac aag tac ttc ggt cga gat ctg aaa	393
Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp Leu Lys	
100 105 110	
gca gga aaa gaa ttt cag gac gcg ctt aag cgc ttt ttt tgg gat ggg	441
Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp Asp Gly	
115 120 125 130	
acg agc tac aaa gca gca aac aga cac ata ccc gtc ata ttg gag aag	489
Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu Glu Lys	
135 140 145	
atc agc caa ctg gaa cgc atg ata cga aaa ctt cca gga tac aga ttc	537
Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr Arg Phe	
150 155 160	
tac gcg agt agt ttg ttg atg ctc tat gat cgt ggg gac ggt gag tcg	585
Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly Glu Ser	
165 170 175	
aag gag aaa gac gca gca ccc tct tta cct aac ggc ttg tcg aac ccg	633
Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser Asn Pro	
180 185 190	
agc aac gaa gac gtt tca aca ata cca tct gga ctt aca tca cca ggg	681
Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser Pro Gly	
195 200 205 210	
ccg aca gtc gct tct aaa ccg tca ccc aag aag cac gga gag atc aag	729
Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu Ile Lys	
215 220 225	
ctg aaa att gtc gac ttt gcc aac tgc gtg act gca gaa gac cct cta	777
Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp Pro Leu	
230 235 240	
cca gac gac tta cct tgt cca cct gaa aat ccc gac ggc atc gat aga	825
Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile Asp Arg	
245 250 255	
ggg tac ctc cgt ggc ctc cga tca cta cgc ctc tac ttc caa cgc att	873
Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln Arg Ile	

260	265	270	
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Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly Glu Gly			
275	280	285	290
atg gcg cga aat cat cac cat ggc cct ggt tta ggt gag gtt ggt gcg			969
Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val Gly Ala			
295	300		305
ggc tgg atg gat gat gct ggt ggt gag gat aca ggc tac gcc agt ttc			1017
Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala Ser Phe			
310	315		320
taa agaagaggag gaacagcaaa gctgcccacg ctcgacagaa gtcggacagt			1070
*			
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Val Gln His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg			
35 40 45			
Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu			
50 55 60			
Ala Asp Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr			
65 70 75 80			
Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn			
85 90 95			
Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp			
100 105 110			
Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp			
115 120 125			
Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu			
130 135 140			
Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr			
145 150 155 160			
Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly			
165 170 175			
Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser			
180 185 190			
Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser			
195 200 205			

Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu  
 210 215 220  
 Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp  
 225 230 235 240  
 Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile  
 245 250 255  
 Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln  
 260 265 270  
 Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly  
 275 280 285  
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 Ser Phe

<210> 24  
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 <212> DNA  
 <213> Zea mays

<220>  
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 <222> (3)...(953)

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 ttt caa act tac aaa aaa cag agg tat cca tgg gta cag cta gcc gga 95  
 Phe Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly  
 20 25 30  
 cac caa ggc aat ttc aaa gcc ggt ccg gaa cct ggt acg atc ctc aag 143  
 His Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys  
 35 40 45  
 aaa ctt tgt ccc aaa gaa cag ttg tgc ttc caa gtg ctg atg aag gac 191  
 Lys Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp  
 50 55 60  
 gtt ctg aga ccg tac gtg ccc gaa tac aag ggc cac ttg act acc gac 239  
 Val Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp  
 65 70 75  
 gac gga gac cta tat ctt cag cta gaa gac ttg ttg ggt gac ttc act 287  
 Asp Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr  
 80 85 90 95  
 tcg ccg tgc gtc atg gac tgc aag atc ggc gtc agg acg tat ctg gaa 335  
 Ser Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu  
 100 105 110  
 gag gaa ctg gcg aaa gcc aaa gag aaa ccc aag ttg aga aaa gac atg 383  
 Glu Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met





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 <212> PRT  
 <213> Zea mays

<400> 25

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	50					55					60				
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Pro	Cys	Val	Met	Asp	Cys	Lys	Ile	Gly	Val	Arg	Thr	Tyr	Leu	Glu	Glu
			100					105					110		
Glu	Leu	Ala	Lys	Ala	Lys	Glu	Lys	Pro	Lys	Leu	Arg	Lys	Asp	Met	Tyr
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Glu	Lys	Met	Ile	Gln	Ile	Asp	Pro	Asn	Ala	Pro	Ser	Glu	Glu	Glu	His
	130					135					140				
Arg	Leu	Lys	Gly	Val	Thr	Lys	Pro	Arg	Tyr	Met	Val	Trp	Arg	Glu	Thr
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				165					170					175	
Ser	Asp	Gly	Lys	Ser	Ser	Lys	Asp	Phe	Lys	Thr	Thr	Lys	Asn	Arg	Asp
			180					185					190		
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		195					200					205			
Ile	Pro	Lys	Tyr	Ile	Asn	Arg	Leu	Arg	Ala	Ile	Arg	Asp	Ile	Leu	Val
	210					215					220				
Asn	Ser	Lys	Phe	Phe	Thr	His	Glu	Val	Ile	Gly	Ser	Ser	Leu	Leu	
225					230					235				240	
Phe	Val	His	Asp	Ser	Lys	Asn	Ala	Asn	Ile	Trp	Leu	Ile	Asp	Phe	Ala
				245					250					255	
Lys	Thr	Leu	Ile	Leu	Pro	Pro	Asp	Ile	Arg	Ile	Asn	His	Thr	Ser	Glu
			260					265					270		
Trp	Val	Val	Gly	Asn	His	Glu	Asp	Gly	Tyr	Leu	Ile	Gly	Ile	Asn	Asn
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Leu	Leu	Asp	Ile	Phe	Thr	Asp	Met	Asn	Ala	Ala	Thr	Ala	Phe	Pro	Val

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<210> 26  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

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 <222> (1)...(25)

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25

<210> 27  
 <211> 30  
 <212> DNA  
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<220>  
 <221> primer\_bind  
 <222> (1)...(30)

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30

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 <212> DNA  
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36

<210> 29  
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<220>  
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 Gln

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 Gln

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 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
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<400> 35

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Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
      35           40
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Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
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      20           25           30
Ile Xaa Lys Cys Leu Xaa Lys Asp Arg
      35           40
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